

## SEQUENCE LISTING

<110> COLE, Stewart  
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GARNIER, Thierry

<120> DELETED SEQUENCE IN M. TUBERCULOSIS, METHOD FOR  
DETECTING MYCOBACTERIA USING THESE SEQUENCES AND  
VACCINES

<130> 346 379- US

<150> PCT/IB 03/00 986

<151> 2003-02-25

<150> EP 02/290 458

<151> 2002-02-25

<160> 22

<170> PatentIn Ver. 2.1

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<213> Mycobacterium tuberculosis strain 74 ("ancestral" strain)

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Phe Val Phe Ser Asp Leu Arg Val Leu Gly Gln Ile Gly Thr Thr Ile  
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 Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln  
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 Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val  
                     115                    120                    125  
 Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu  
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 Asp Lys Ser Ser  
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 <212> DNA  
 <213> Mycobacterium tuberculosis strain 74 ("ancestral" strain).

<220>  
 <223> Sequence specifically deleted in "modern" strains of  
 Mycobacterium tuberculosis

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 aaccccaaac aggtaacctt cgaggtcttt ggcgctcccg gaaccgtggc aacgatcaat 180  
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 tccatcggtt gccgcatcac cgtcaacggt gtagtcaagg acgaaaggat cgtcaacgaa 360  
 gtgcgcgcct ataccttctg cctcgacaag tctcatgag caacaccac cgcccgcggc 420  
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 tcgcacagag ctccccgat gaccgctcgc tgcaggcgat gaaacgcac ggcaagggtg 600  
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 gcaacgacgc ccaccggttc tacgacaccc tgctccgcaa cctttcaaac gacaccaaac 720  
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 tataccgttc cgtcgtcacc atggctcttg tgcttatcac ggttcttatt gagttggccg 1080  
 cggcccgcg gatcgtcgt tttctcgga acgcgggggt aatcgggctg tcgacatact 1140  
 cgacgaatct gctcacaacta ttggtaatcg cggcgggcac agactacgcg atttttgtcc 1200  
 tcggccgcta tcacgaggcg cgctacgcgc cacaggatcg ggaaacggcc ttctacacga 1260  
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 cggtaaacga actgcgagat aggatcgcca atttcgacga tttcttcagg ccgattcgta 2100  
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<220>  
 <223> mmpL6 coding sequence and protein

<220>  
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Arg Leu Ser Leu Pro Ile Leu Leu Phe Trp Val Gly Val Ala Ala Ile	
20 25 30	
acc aat gcc gcc gtg ccg caa ttg gag gtg gtc ggg gag gcg cat aac	144
Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly Glu Ala His Asn	
35 40 45	
gtc gca cag agc tcc ccg gat gac ccg tcg ctg cag gcg atg aaa cgc	192
Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg	
50 55 60	
atc ggc aag gtg ttc cac gag ttc gat tcc gac agt gcg gcc atg atc	240
Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile	
65 70 75 80	
gtc ttg gaa ggc gat aag ccg ctc ggc aac gac gcc cac ccg ttc tac	288
Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala His Arg Phe Tyr	
85 90 95	
gac acc ctg ctc cgc aac ctt tca aac gac acc aaa cac gtc gag cac	336
Asp Thr Leu Leu Arg Asn Leu Ser Asn Asp Thr Lys His Val Glu His	
100 105 110	
gtt cag gac ttc tgg ggc gat ccg ctg acc gcg gcc ggc tcg caa agc	384
Val Gln Asp Phe Trp Gly Asp Pro Leu Thr Ala Ala Gly Ser Gln Ser	
115 120 125	
acc gac ggc aaa gcc gcc tac gtt cag gtc tat ctc gcc ggc aac caa	432
Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu Ala Gly Asn Gln	
130 135 140	
ggc gag gcg ttg tca atc gag tcc gtc gac gcg gtg cgc gac atc gtc	480
Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val Arg Asp Ile Val	
145 150 155 160	
gcc cat acg cca cca ccg gcc ggg gtc aag gcc tac gtc acc ggc gcg	528
Ala His Thr Pro Pro Ala Gly Val Lys Ala Tyr Val Thr Gly Ala	
165 170 175	
gcc ccg ctc atg gcc gat cag ttt cag gtg ggc agc aaa gga acc gcg	576
Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser Lys Gly Thr Ala	
180 185 190	
aaa gtt acc ggg ata act ctg gtt gtg atc gcg gtg atg ttg ctc ttc	624
Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val Met Leu Leu Phe	
195 200 205	
gta tac cgt tcc gtc gtc acc atg gtc ctg gtg ctt atc acg gtt ctt	672
Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu Ile Thr Val Leu	
210 215 220	
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Ile Glu Leu Ala Ala Ala Arg Gly Ile Val Ala Phe Leu Gly Asn Ala	
225 230 235 240	

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Gly Val Ile Gly Leu Ser Thr Tyr Ser Thr Asn Leu Leu Thr Leu Leu	
245 250 255	
gta atc gcg gcg ggc aca gac tac gcg att ttt gtc ctc ggc cgc tat	816
Val Ile Ala Ala Gly Thr Asp Tyr Ala Ile Phe Val Leu Gly Arg Tyr	
260 265 270	
cac gag gcg cgc tac gcc gca cag gat cgg gaa acg gcc ttc tac acg	864
His Glu Ala Arg Tyr Ala Ala Gln Asp Arg Glu Thr Ala Phe Tyr Thr	
275 280 285	
atg tat cgc ggg acc gcc cac gtc gtc ttg ggc tctg ggt ctg acc gtt	912
Met Tyr Arg Gly Thr Ala His Val Val Leu Gly Ser Gly Leu Thr Val	
290 295 300	
gcc ggc gcg gtg tat tgc ctg agc ttt acc cgg cta ccc tat ttt caa	960
Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln	
305 310 315 320	
agc ctg ggt att ccc gcc tctg ata ggg gtg atg att gcg ttg gca gcc	1008
Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala	
325 330 335	
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Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly Ser Arg Phe Gly	
340 345 350	
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Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile	
355 360 365	
ggc acg gcc atc gtg cgt tgg ccg gga ccc atc ctg gca gtg gcg tgc	1152
Gly Thr Ala Ile Val Arg Trp Pro Gly Pro Ile Leu Ala Val Ala Cys	
370 375 380	
gca att gcg gtg gtg ggt ctg ctc gcg ctg ccg gga tac aaa acg agc	1200
Ala Ile Ala Val Val Gly Leu Leu Ala Leu Pro Gly Tyr Lys Thr Ser	
385 390 395 400	
tac gac gct cgc tat tac atg ccc gcc acc gcc ccg gcc aat att ggc	1248
Tyr Asp Ala Arg Tyr Tyr Met Pro Ala Thr Ala Pro Ala Asn Ile Gly	
405 410 415	
tac atg gcc gcg gag cga cat ttt ccc caa gcg cgg ctg aat ccc gaa	1296
Tyr Met Ala Ala Glu Arg His Phe Pro Gln Ala Arg Leu Asn Pro Glu	
420 425 430	
cta ctg atg atc gag acg gat cac gat atg cgc aat ccg gcc gac atg	1344
Leu Leu Met Ile Glu Thr Asp His Asp Met Arg Asn Pro Ala Asp Met	
435 440 445	
ctc atc ttg gat agg atc gcc aag gct gtc ttc cat ctg ccc ggc ata	1392
Leu Ile Leu Asp Arg Ile Ala Lys Ala Val Phe His Leu Pro Gly Ile	
450 455 460	
ggg ctg gtg cag gcc atg acc cgg ccg cta gga acc ccg att gac cac	1440
Gly Leu Val Gln Ala Met Thr Arg Pro Leu Gly Thr Pro Ile Asp His	
465 470 475 480	

agc tgc ata ccg ttt cag atc agc atg caa agc gtc ggc cag att cag	1488
Ser Ser Ile Pro Phe Gln Ile Ser Met Gln Ser Val Gly Gln Ile Gln	
485 490 495	
aat ctc aag tat cag agg gac cga gca gcc gac ttg ctg aag cag gcc	1536
Asn Leu Lys Tyr Gln Arg Asp Arg Ala Ala Asp Leu Leu Lys Gln Ala	
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gaa gag ctg ggg aag acg atc gaa atc ttg cag cgc caa tat gcc cta	1584
Glu Glu Leu Gly Lys Thr Ile Glu Ile Leu Gln Arg Gln Tyr Ala Leu	
515 520 525	
cag cag gaa ctc gcg gcc gct act cac gag caa gcc gaa agc ttt cac	1632
Gln Gln Glu Leu Ala Ala Thr His Glu Gln Ala Glu Ser Phe His	
530 535 540	
caa acg atc gcc acg gta aag gaa ctg cga gat agg atc gcc aat ttc	1680
Gln Thr Ile Ala Thr Val Lys Glu Leu Arg Asp Arg Ile Ala Asn Phe	
545 550 555 560	
gac gat ttc ttc agg ccg att cgt agt tac ttt tac tgg gaa aag cac	1728
Asp Asp Phe Phe Arg Pro Ile Arg Ser Tyr Phe Tyr Trp Glu Lys His	
565 570 575	
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Cys Tyr Asp Ile Pro Ser Cys Trp Ala Leu Arg Ser Val Phe Asp Thr	
580 585 590	
atc gac ggt atc gac caa ctc ggc gag cag ctg gcc agc gtg acc gta	1824
Ile Asp Gly Ile Asp Gln Leu Gly Glu Gln Leu Ala Ser Val Thr Val	
595 600 605	
acc ttg gac aag ttg gct gcg atc cag cct caa ttg gtg gcg ctg cta	1872
Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro Gln Leu Val Ala Leu Leu	
610 615 620	
cca gac gag atc gcc agc cag cag atc aat cgg gaa ctg gcg ctg gct	1920
Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn Arg Glu Leu Ala Leu Ala	
625 630 635 640	
aac tac gcc acc atg tcc ggg atc tat gcc cag acg gcg gcc ttg atc	1968
Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala Gln Thr Ala Ala Leu Ile	
645 650 655	
gaa aac gct gcc gcc atg gga caa gcc ttt gac gcc gcc aag aac gac	2016
Glu Asn Ala Ala Ala Met Gly Gln Ala Phe Asp Ala Ala Lys Asn Asp	
660 665 670	
gac tcc ttc tat ctg ccg ccg gag gct ttt gac aac cca gat ttc cag	2064
Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe Asp Asn Pro Asp Phe Gln	
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cgc ggc ctg aaa ttg ttc ctg tgc gca gac ggt aag gcg gct cgg atg	2112
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atc atc tcc cat gaa ggc gat ccc gcc acc ccc gaa ggc att tgc cat	2160
Ile Ile Ser His Glu Gly Asp Pro Ala Thr Pro Glu Gly Ile Ser His	
705 710 715 720	
atc gac gcg atc aag cag gcg gcc cac gag gcc gtg aag ggc act ccc	2208

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Met	Ala	Gly	Ala	Gly	Ile	Tyr	Leu	Ala	Gly	Thr	Ala	Ala	Thr	Phe	Lys		
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gac	att	caa	gac	ggc	gcc	acc	tac	gac	ctc	ctg	atc	gcc	gga	ata	gcc	2304	
Asp	Ile	Gln	Asp	Gly	Ala	Thr	Tyr	Asp	Leu	Leu	Ile	Ala	Gly	Ile	Ala		
				755					760				765				
gcg	ctg	agc	ttg	att	ttg	ctc	atc	atg	atg	atc	att	acc	cga	agc	ctg	2352	
Ala	Leu	Ser	Leu	Ile	Leu	Leu	Ile	Met	Met	Ile	Ile	Thr	Arg	Ser	Leu		
				770					775				780				
gtt	gcg	gcg	ctg	gtg	atc	gtg	ggc	acg	gtg	gcg	ctg	tcg	ttg	ggc	gct	2400	
Val	Ala	Ala	Leu	Val	Ile	Val	Gly	Thr	Val	Ala	Leu	Ser	Leu	Gly	Ala		
				785					790				795				
tct	ttt	ggc	ctg	tcc	gtg	ctg	gtg	tgg	cag	cat	ctt	ctc	ggt	atc	cag	2448	
Ser	Phe	Gly	Leu	Ser	Val	Leu	Val	Trp	Gln	His	Leu	Leu	Gly	Ile	Gln		
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ttg	tac	tgg	atc	gtg	ctc	gcg	ctg	gcc	gtc	atc	ctg	ctc	ctg	gcc	gtg	2496	
Leu	Tyr	Trp	Ile	Val	Leu	Ala	Leu	Ala	Val	Ile	Leu	Leu	Leu	Ala	Val		
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Gly	Ser	Asp	Tyr	Asn	Leu	Leu	Leu	Ile	Ser	Arg	Phe	Lys	Glu	Glu	Ile		
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ggt	gca	ggt	ttg	aac	acc	ggc	atc	atc	cgt	gcg	atg	gcc	ggc	acc	ggc	2592	
Gly	Ala	Gly	Leu	Asn	Thr	Gly	Ile	Ile	Arg	Ala	Met	Ala	Gly	Thr	Gly		
				850					855				860				
ggg	gtg	gtg	acc	gct	gcc	ggc	ctg	gtg	ttc	gcc	gcc	act	atg	tct	tcg	2640	
Gly	Val	Val	Thr	Ala	Ala	Gly	Leu	Val	Phe	Ala	Ala	Thr	Met	Ser	Ser		
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ttc	gtg	ttc	agt	gat	ttg	cgg	gtc	ctc	ggt	cag	atc	ggg	acc	acc	att	2688	
Phe	Val	Phe	Ser	Asp	Leu	Arg	Val	Leu	Gly	Gln	Ile	Gly	Thr	Thr	Ile		
				885					890				895				
ggt	ctt	ggg	ctg	ctg	ttc	gac	acg	ctg	gtg	gtg	cgc	gcg	ttc	atg	acc	2736	
Gly	Leu	Gly	Leu	Leu	Phe	Asp	Thr	Leu	Val	Val	Arg	Ala	Phe	Met	Thr		
				900					905				910				
ccg	tcc	atc	gcg	gtg	ctg	ctc	ggg	cgc	tgg	ttc	tgg	tgg	ccg	caa	cga	2784	
Pro	Ser	Ile	Ala	Val	Leu	Leu	Gly	Arg	Trp	Phe	Trp	Trp	Pro	Gln	Arg		
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gtg	cgc	ccg	cgc	cct	gcc	agc	agg	atg	ctt	cgg	ccg	tac	ggc	ccg	cgg	2832	
Val	Arg	Pro	Arg	Pro	Ala	Ser	Arg	Met	Leu	Arg	Pro	Tyr	Gly	Pro	Arg		
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ccc	gtg	gtt	cgt	gaa	ttg	ctg	ctg	cgc	gag	ggc	aac	gat	gac	ccg	aga	2880	
Pro	Val	Val	Arg	Glu	Leu	Leu	Leu	Arg	Glu	Gly	Asn	Asp	Asp	Pro	Arg		
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965

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<220>  
 <223> mmpL6 protein

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 Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly Glu Ala His Asn  
 35 40 45  
 Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg  
 50 55 60  
 Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile  
 65 70 75 80  
 Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala His Arg Phe Tyr  
 85 90 95  
 Asp Thr Leu Leu Arg Asn Leu Ser Asn Asp Thr Lys His Val Glu His  
 100 105 110  
 Val Gln Asp Phe Trp Gly Asp Pro Leu Thr Ala Ala Gly Ser Gln Ser  
 115 120 125  
 Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu Ala Gly Asn Gln  
 130 135 140  
 Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val Arg Asp Ile Val  
 145 150 155 160  
 Ala His Thr Pro Pro Pro Ala Gly Val Lys Ala Tyr Val Thr Gly Ala  
 165 170 175  
 Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser Lys Gly Thr Ala  
 180 185 190  
 Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val Met Leu Leu Phe  
 195 200 205  
 Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu Ile Thr Val Leu  
 210 215 220  
 Ile Glu Leu Ala Ala Ala Arg Gly Ile Val Ala Phe Leu Gly Asn Ala  
 225 230 235 240  
 Gly Val Ile Gly Leu Ser Thr Tyr Ser Thr Asn Leu Leu Thr Leu Leu  
 245 250 255

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His	Glu	Ala	Arg	Tyr	Ala	Ala	Gln	Asp	Arg	Glu	Thr	Ala	Phe	Tyr	Thr
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Met	Tyr	Arg	Gly	Thr	Ala	His	Val	Val	Leu	Gly	Ser	Gly	Leu	Thr	Val
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Ser	Leu	Gly	Ile	Pro	Ala	Ser	Ile	Gly	Val	Met	Ile	Ala	Leu	Ala	Ala
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Cys	Phe	Glu	Pro	Lys	Arg	Arg	Met	Arg	Thr	Arg	Gly	Trp	Arg	Arg	Ile
		355				360						365			
Gly	Thr	Ala	Ile	Val	Arg	Trp	Pro	Gly	Pro	Ile	Leu	Ala	Val	Ala	Cys
		370				375				380					
Ala	Ile	Ala	Val	Val	Gly	Leu	Leu	Ala	Leu	Pro	Gly	Tyr	Lys	Thr	Ser
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Tyr	Asp	Ala	Arg	Tyr	Tyr	Met	Pro	Ala	Thr	Ala	Pro	Ala	Asn	Ile	Gly
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Tyr	Met	Ala	Ala	Glu	Arg	His	Phe	Pro	Gln	Ala	Arg	Leu	Asn	Pro	Glu
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Leu	Leu	Met	Ile	Glu	Thr	Asp	His	Asp	Met	Arg	Asn	Pro	Ala	Asp	Met
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Gly	Leu	Val	Gln	Ala	Met	Thr	Arg	Pro	Leu	Gly	Thr	Pro	Ile	Asp	His
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Ser	Ser	Ile	Pro	Phe	Gln	Ile	Ser	Met	Gln	Ser	Val	Gly	Gln	Ile	Gln
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Glu	Glu	Leu	Gly	Lys	Thr	Ile	Glu	Ile	Leu	Gln	Arg	Gln	Tyr	Ala	Leu
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Gln	Gln	Glu	Leu	Ala	Ala	Ala	Thr	His	Glu	Gln	Ala	Glu	Ser	Phe	His
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Gln	Thr	Ile	Ala	Thr	Val	Lys	Glu	Leu	Arg	Asp	Arg	Ile	Ala	Asn	Phe
		545				550				555				560	
Asp	Asp	Phe	Phe	Arg	Pro	Ile	Arg	Ser	Tyr	Phe	Tyr	Trp	Glu	Lys	His
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Cys	Tyr	Asp	Ile	Pro	Ser	Cys	Trp	Ala	Leu	Arg	Ser	Val	Phe	Asp	Thr



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Ile	Asp	Gly	Ile	Asp	Gln	Leu	Gly	Glu	Gln	Leu	Ala	Ser	Val	Thr	Val
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Thr	Leu	Asp	Lys	Leu	Ala	Ala	Ile	Gln	Pro	Gln	Leu	Val	Ala	Leu	Leu
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Asn	Tyr	Ala	Thr	Met	Ser	Gly	Ile	Tyr	Ala	Gln	Thr	Ala	Ala	Leu	Ile
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Glu	Asn	Ala	Ala	Ala	Met	Gly	Gln	Ala	Phe	Asp	Ala	Ala	Lys	Asn	Asp
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Asp	Ser	Phe	Tyr	Leu	Pro	Pro	Glu	Ala	Phe	Asp	Asn	Pro	Asp	Phe	Gln
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Arg	Gly	Leu	Lys	Leu	Phe	Leu	Ser	Ala	Asp	Gly	Lys	Ala	Ala	Arg	Met
	690					695					700				
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Met	Ala	Gly	Ala	Gly	Ile	Tyr	Leu	Ala	Gly	Thr	Ala	Ala	Thr	Phe	Lys
			740					745					750		
Asp	Ile	Gln	Asp	Gly	Ala	Thr	Tyr	Asp	Leu	Leu	Ile	Ala	Gly	Ile	Ala
		755					760					765			
Ala	Leu	Ser	Leu	Ile	Leu	Leu	Ile	Met	Met	Ile	Ile	Thr	Arg	Ser	Leu
	770					775					780				
Val	Ala	Ala	Leu	Val	Ile	Val	Gly	Thr	Val	Ala	Leu	Ser	Leu	Gly	Ala
785						790					795				800
Ser	Phe	Gly	Leu	Ser	Val	Leu	Val	Trp	Gln	His	Leu	Leu	Gly	Ile	Gln
				805					810					815	
Leu	Tyr	Trp	Ile	Val	Leu	Ala	Leu	Ala	Val	Ile	Leu	Leu	Leu	Ala	Val
			820					825					830		
Gly	Ser	Asp	Tyr	Asn	Leu	Leu	Leu	Ile	Ser	Arg	Phe	Lys	Glu	Glu	Ile
		835					840					845			
Gly	Ala	Gly	Leu	Asn	Thr	Gly	Ile	Ile	Arg	Ala	Met	Ala	Gly	Thr	Gly
	850					855					860				
Gly	Val	Val	Thr	Ala	Ala	Gly	Leu	Val	Phe	Ala	Ala	Thr	Met	Ser	Ser
865						870					875				880
Phe	Val	Phe	Ser	Asp	Leu	Arg	Val	Leu	Gly	Gln	Ile	Gly	Thr	Thr	Ile
				885					890					895	
Gly	Leu	Gly	Leu	Leu	Phe	Asp	Thr	Leu	Val	Val	Arg	Ala	Phe	Met	Thr

900	905	910
Pro Ser Ile Ala Val Leu Leu Gly Arg Trp Phe Trp Trp Pro Gln Arg		
915	920	925
Val Arg Pro Arg Pro Ala Ser Arg Met Leu Arg Pro Tyr Gly Pro Arg		
930	935	940
Pro Val Val Arg Glu Leu Leu Leu Arg Glu Gly Asn Asp Asp Pro Arg		
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Thr Gln Val Ala Thr His Arg		
965		

<210> 7  
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 <212> DNA  
 <213> Mycobacterium complex

<220>  
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 <222> (1)..(1758)

<220>  
 <223> mmpL6 truncated coding sequence and protein

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Met Ser Asn His His Arg Pro Arg Pro Trp Leu Pro His Thr Ile Arg	
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cgg ctt tcg ttg ccg atc ttg ctg ttt tgg gtg ggt gtg gcc gcc ata	96
Arg Leu Ser Leu Pro Ile Leu Leu Phe Trp Val Gly Val Ala Ala Ile	
20 25 30	
acc aat gcc gcc gtg ccg caa ttg gag gtg gtc ggg gag gcg cat aac	144
Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly Glu Ala His Asn	
35 40 45	
gtc gca cag agc tcc ccg gat gac ccg tcg ctg cag gcg atg aaa cgc	192
Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg	
50 55 60	
atc ggc aag gtg ttc cac gag ttc gat tcc gac agt gcg gcc atg atc	240
Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile	
65 70 75 80	
gtc ttg gaa ggc gat aag ccg ctc ggc aac gac gcc cac cgg ttc tac	288
Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala His Arg Phe Tyr	
85 90 95	
gac acc ctg ctc cgc aac ctt tca aac gac acc aaa cac gtc gag cac	336
Asp Thr Leu Leu Arg Asn Leu Ser Asn Asp Thr Lys His Val Glu His	
100 105 110	
gtt cag gac ttc tgg ggc gat ccg ctg acc gcg gcc ggc tcg caa agc	384
Val Gln Asp Phe Trp Gly Asp Pro Leu Thr Ala Ala Gly Ser Gln Ser	
115 120 125	

acc gac ggc aaa gcc gcc tac gtt cag gtc tat ctc gcc ggc aac caa	432
Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu Ala Gly Asn Gln	
130 135 140	
ggc gag gcg ttg tca atc gag tcc gtc gac gcg gtg cgc gac atc gtc	480
Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val Arg Asp Ile Val	
145 150 155 160	
gcc cat acg cca cca ccg gcc ggg gtc aag gcc tac gtc acc ggc gcg	528
Ala His Thr Pro Pro Pro Ala Gly Val Lys Ala Tyr Val Thr Gly Ala	
165 170 175	
gcc ccg ctc atg gcc gat cag ttt cag gtg ggc agc aaa gga acc gcg	576
Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser Lys Gly Thr Ala	
180 185 190	
aaa gtt acc ggg ata act ctg gtt gtg atc gcg gtg atg ttg ctc ttc	624
Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val Met Leu Leu Phe	
195 200 205	
gta tac cgt tcc gtc gtc acc atg gtc ctg gtg ctt atc acg gtt ctt	672
Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu Ile Thr Val Leu	
210 215 220	
att gag ttg gcc gcg gcc cgc ggg atc gtc gct ttt ctc gga aac gcc	720
Ile Glu Leu Ala Ala Ala Arg Gly Ile Val Ala Phe Leu Gly Asn Ala	
225 230 235 240	
ggg gta atc ggg ctg tcg aca tac tcg acg aat ctg ctc aca cta ttg	768
Gly Val Ile Gly Leu Ser Thr Tyr Ser Thr Asn Leu Leu Thr Leu Leu	
245 250 255	
gta atc gcg gcg ggc aca gac tac gcg att ttt gtc ctc ggc cgc tat	816
Val Ile Ala Ala Gly Thr Asp Tyr Ala Ile Phe Val Leu Gly Arg Tyr	
260 265 270	
cac gag gcg cgc tac gcc gca cag gat cgg gaa acg gcc ttc tac acg	864
His Glu Ala Arg Tyr Ala Ala Gln Asp Arg Glu Thr Ala Phe Tyr Thr	
275 280 285	
atg tat cgc ggg acc gcc cac gtc gtc ttg ggc tcg ggt ctg acc gtt	912
Met Tyr Arg Gly Thr Ala His Val Val Leu Gly Ser Gly Leu Thr Val	
290 295 300	
gcc ggc gcg gtg tat tgc ctg agc ttt acc cgg cta ccc tat ttt caa	960
Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln	
305 310 315 320	
agc ctg ggt att ccc gcc tcg ata ggg gtg atg att gcg ttg gca gcc	1008
Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala	
325 330 335	
gcg ctc agc ctg gcc cca tcc gtg ctc atc ttg ggc agt cgt ttc ggt	1056
Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly Ser Arg Phe Gly	
340 345 350	
tgt ttc gaa ccc aag cgc agg atg agg acc agg gga tgg cgg cgc atc	1104
Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile	
355 360 365	
ggc acg gcc atc gtg cgt tgg ccg gga ccc atc ctg gca gtg gcg tgc	1152

Gly	Thr	Ala	Ile	Val	Arg	Trp	Pro	Gly	Pro	Ile	Leu	Ala	Val	Ala	Cys.		
370						375					380						
gca	att	gcg	gtg	gtg	ggt	ctg	ctc	gcg	ctg	ccg	gga	tac	aaa	acg	agc	1200	
Ala	Ile	Ala	Val	Val	Gly	Leu	Leu	Ala	Leu	Pro	Gly	Tyr	Lys	Thr	Ser		
385					390					395					400		
tac	gac	gct	cgc	tat	tac	atg	ccc	gcc	acc	gcc	ccg	gcc	aat	att	ggc	1248	
Tyr	Asp	Ala	Arg	Tyr	Tyr	Met	Pro	Ala	Thr	Ala	Pro	Ala	Asn	Ile	Gly		
				405					410					415			
tac	atg	gcc	gcg	gag	cga	cat	ttt	ccc	caa	gcg	cgg	ctg	aat	ccc	gaa	1296	
Tyr	Met	Ala	Ala	Glu	Arg	His	Phe	Pro	Gln	Ala	Arg	Leu	Asn	Pro	Glu		
				420				425						430			
cta	ctg	atg	atc	gag	acg	gat	cac	gat	atg	cgc	aat	ccg	gcc	gac	atg	1344	
Leu	Leu	Met	Ile	Glu	Thr	Asp	His	Asp	Met	Arg	Asn	Pro	Ala	Asp	Met		
		435					440					445					
ctc	atc	ttg	gat	agg	atc	gcc	aag	gct	gtc	ttc	cat	ctg	ccc	ggc	ata	1392	
Leu	Ile	Leu	Asp	Arg	Ile	Ala	Lys	Ala	Val	Phe	His	Leu	Pro	Gly	Ile		
		450				455					460						
ggg	ctg	gtg	cag	gcc	atg	acc	cgg	ccg	cta	gga	acc	ccg	att	gac	cac	1440	
Gly	Leu	Val	Gln	Ala	Met	Thr	Arg	Pro	Leu	Gly	Thr	Pro	Ile	Asp	His		
465					470					475					480		
agc	tcg	ata	ccg	ttt	cag	atc	agc	atg	caa	agc	gtc	ggc	cag	att	cag	1488	
Ser	Ser	Ile	Pro	Phe	Gln	Ile	Ser	Met	Gln	Ser	Val	Gly	Gln	Ile	Gln		
				485				490						495			
aat	ctc	aag	tat	cag	agg	gac	cga	gca	gcc	gac	ttg	ctg	aag	cag	gcc	1536	
Asn	Leu	Lys	Tyr	Gln	Arg	Asp	Arg	Ala	Ala	Asp	Leu	Leu	Lys	Gln	Ala		
			500					505						510			
gaa	gag	ctg	ggg	aag	acg	atc	gaa	atc	ttg	cag	cgc	caa	tat	gcc	cta	1584	
Glu	Glu	Leu	Gly	Lys	Thr	Ile	Glu	Ile	Leu	Gln	Arg	Gln	Tyr	Ala	Leu		
		515					520					525					
cag	cag	gaa	ctc	gcg	gcc	gct	act	cac	gag	caa	gcc	gaa	agc	ttt	cac	1632	
Gln	Gln	Glu	Leu	Ala	Ala	Ala	Thr	His	Glu	Gln	Ala	Glu	Ser	Phe	His		
		530				535					540						
caa	acg	atc	gcc	acg	gta	aag	gaa	ctg	cga	gat	agg	atc	gcc	aat	ttc	1680	
Gln	Thr	Ile	Ala	Thr	Val	Lys	Glu	Leu	Arg	Asp	Arg	Ile	Ala	Asn	Phe		
545					550					555					560		
gac	gat	ttc	ttc	agg	ccg	att	cgt	agt	tac	ttt	tac	tgg	gaa	aag	cac	1728	
Asp	Asp	Phe	Phe	Arg	Pro	Ile	Arg	Ser	Tyr	Phe	Tyr	Trp	Glu	Lys	His		
				565				570						575			
tgc	tac	gat	atc	ccg	agc	tgc	tgg	gcg	ctg							1758	
Cys	Tyr	Asp	Ile	Pro	Ser	Cys	Trp	Ala	Leu								
			580					585									

&lt;210&gt; 8

&lt;211&gt; 586

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium complex

&lt;220&gt;

&lt;223&gt; mmpL6 truncated protein

&lt;400&gt; 8

Met	Ser	Asn	His	His	Arg	Pro	Arg	Pro	Trp	Leu	Pro	His	Thr	Ile	Arg	1	5	10	15
Arg	Leu	Ser	Leu	Pro	Ile	Leu	Leu	Phe	Trp	Val	Gly	Val	Ala	Ala	Ile	20	25	30	
Thr	Asn	Ala	Ala	Val	Pro	Gln	Leu	Glu	Val	Val	Gly	Glu	Ala	His	Asn	35	40	45	
Val	Ala	Gln	Ser	Ser	Pro	Asp	Asp	Pro	Ser	Leu	Gln	Ala	Met	Lys	Arg	50	55	60	
Ile	Gly	Lys	Val	Phe	His	Glu	Phe	Asp	Ser	Asp	Ser	Ala	Ala	Met	Ile	65	70	75	80
Val	Leu	Glu	Gly	Asp	Lys	Pro	Leu	Gly	Asn	Asp	Ala	His	Arg	Phe	Tyr	85	90	95	
Asp	Thr	Leu	Leu	Arg	Asn	Leu	Ser	Asn	Asp	Thr	Lys	His	Val	Glu	His	100	105	110	
Val	Gln	Asp	Phe	Trp	Gly	Asp	Pro	Leu	Thr	Ala	Ala	Gly	Ser	Gln	Ser	115	120	125	
Thr	Asp	Gly	Lys	Ala	Ala	Tyr	Val	Gln	Val	Tyr	Leu	Ala	Gly	Asn	Gln	130	135	140	
Gly	Glu	Ala	Leu	Ser	Ile	Glu	Ser	Val	Asp	Ala	Val	Arg	Asp	Ile	Val	145	150	155	160
Ala	His	Thr	Pro	Pro	Pro	Ala	Gly	Val	Lys	Ala	Tyr	Val	Thr	Gly	Ala	165	170	175	
Ala	Pro	Leu	Met	Ala	Asp	Gln	Phe	Gln	Val	Gly	Ser	Lys	Gly	Thr	Ala	180	185	190	
Lys	Val	Thr	Gly	Ile	Thr	Leu	Val	Val	Ile	Ala	Val	Met	Leu	Leu	Phe	195	200	205	
Val	Tyr	Arg	Ser	Val	Val	Thr	Met	Val	Leu	Val	Leu	Ile	Thr	Val	Leu	210	215	220	
Ile	Glu	Leu	Ala	Ala	Ala	Arg	Gly	Ile	Val	Ala	Phe	Leu	Gly	Asn	Ala	225	230	235	240
Gly	Val	Ile	Gly	Leu	Ser	Thr	Tyr	Ser	Thr	Asn	Leu	Leu	Thr	Leu	Leu	245	250	255	
Val	Ile	Ala	Ala	Gly	Thr	Asp	Tyr	Ala	Ile	Phe	Val	Leu	Gly	Arg	Tyr	260	265	270	
His	Glu	Ala	Arg	Tyr	Ala	Ala	Gln	Asp	Arg	Glu	Thr	Ala	Phe	Tyr	Thr	275	280	285	
Met	Tyr	Arg	Gly	Thr	Ala	His	Val	Val	Leu	Gly	Ser	Gly	Leu	Thr	Val	290	295	300	

Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln  
 305 310 315 320  
 Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala  
 325 330 335  
 Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly Ser Arg Phe Gly  
 340 345 350  
 Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile  
 355 360 365  
 Gly Thr Ala Ile Val Arg Trp Pro Gly Pro Ile Leu Ala Val Ala Cys  
 370 375 380  
 Ala Ile Ala Val Val Gly Leu Leu Ala Leu Pro Gly Tyr Lys Thr Ser  
 385 390 395 400  
 Tyr Asp Ala Arg Tyr Tyr Met Pro Ala Thr Ala Pro Ala Asn Ile Gly  
 405 410 415  
 Tyr Met Ala Ala Glu Arg His Phe Pro Gln Ala Arg Leu Asn Pro Glu  
 420 425 430  
 Leu Leu Met Ile Glu Thr Asp His Asp Met Arg Asn Pro Ala Asp Met  
 435 440 445  
 Leu Ile Leu Asp Arg Ile Ala Lys Ala Val Phe His Leu Pro Gly Ile  
 450 455 460  
 Gly Leu Val Gln Ala Met Thr Arg Pro Leu Gly Thr Pro Ile Asp His  
 465 470 475 480  
 Ser Ser Ile Pro Phe Gln Ile Ser Met Gln Ser Val Gly Gln Ile Gln  
 485 490 495  
 Asn Leu Lys Tyr Gln Arg Asp Arg Ala Ala Asp Leu Leu Lys Gln Ala  
 500 505 510  
 Glu Glu Leu Gly Lys Thr Ile Glu Ile Leu Gln Arg Gln Tyr Ala Leu  
 515 520 525  
 Gln Gln Glu Leu Ala Ala Ala Thr His Glu Gln Ala Glu Ser Phe His  
 530 535 540  
 Gln Thr Ile Ala Thr Val Lys Glu Leu Arg Asp Arg Ile Ala Asn Phe  
 545 550 555 560  
 Asp Asp Phe Phe Arg Pro Ile Arg Ser Tyr Phe Tyr Trp Glu Lys His  
 565 570 575  
 Cys Tyr Asp Ile Pro Ser Cys Trp Ala Leu  
 580 585

&lt;210&gt; 9

&lt;211&gt; 447

&lt;212&gt; DNA

&lt;213&gt; Mycobacterium complex

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<222> (1) .. (444)
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<223> mmpS6 coding sequence and protein

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Val	Gln	Gly	Ile	Ser	Val	Thr	Gly	Leu	Val	Lys	Arg	Gly	Trp	Met	Val	
1				5					10					15		

ctg gtt gcc gtg gcg gtg gtg gcg gtc gcg gga ttc agc gtc tat cgg 96  
Leu Val Ala Val Ala Val Val Ala Val Ala Gly Phe Ser Val Tyr Arg  
20 25 30

ttg cac ggc atc ttc ggc tcg cac gac acc acc tcg acc gcc ggt ggt 144  
Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly  
35 40 45

gtc gcg aac gac atc aag ccg ttc aac ccc aaa cag gta acc ctc gag 192  
Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu  
50 55 60

gtc ttt ggc gct ccc gga acc gtg gca acg atc aat tat ctg gac gtg 240  
Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val  
65 70 75 80

gat gcc aca cct cgg caa gtc ctg gac acg acc ctg cgg tgg tca tac 288  
Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr  
85 90 95

acg atc acg acg acc ctg ccc gcg gtc ttc gcc aat gtt gtc gcg caa 336  
Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln  
100 105 110

ggc gac agc aat tcc atc ggc tgc cgc atc acc gtc aac ggt gta gtc 384  
Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val  
115 120 125

aag gac gaa agg atc gtc aac gaa gtg cgc gcc tat acc ttc tgc ctc 432  
Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu  
130 135 140

gac aag tcc tca tga  
Asp Lys Ser Ser  
145

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<210> 10
<211> 148
<212> PRT
<213> Mycobacterium complex
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<220>  
<223> mmpS6 protein

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Leu Val Ala Val Ala Val Val Ala Val Ala Gly Phe Ser Val Tyr Arg  
                   20                                  25                                  30  
 Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly  
                   35                                  40                                  45  
 Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu  
                   50                                  55                                  60  
 Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val  
                   65                                  70                                  75                                  80  
 Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr  
                                   85                                  90                                  95  
 Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln  
                                   100                                  105                                  110  
 Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val  
                   115                                  120                                  125  
 Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu  
                   130                                  135                                  140  
 Asp Lys Ser Ser  
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<210> 11  
 <211> 399  
 <212> DNA  
 <213> Mycobacterium complex

<220>  
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 <222> (1)..(399)

<220>  
 <223> mmpS6 truncated coding sequence and protein

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 ttg cac ggc atc ttc ggc tcg cac gac acc acc tcg acc gcc ggt ggt 96  
 Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly  
                   20                                  25                                  30  
 gtc gcg aac gac atc aag ccg ttc aac ccc aaa cag gta acc ctc gag 144  
 Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu  
                   35                                  40                                  45  
 gtc ttt ggc gct ccc gga acc gtg gca acg atc aat tat ctg gac gtg 192  
 Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val  
                   50                                  55                                  60  
 gat gcc aca cct cgg caa gtc ctg gac acg acc ctg ccg tgg tca tac 240  
 Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr  
                   65                                  70                                  75                                  80



acg atc acg acg acc ctg ccc gcg gtc ttc gcc aat gtt gtc gcg caa 288  
 Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln  
                     85                    90                    95

ggc gac agc aat tcc atc ggc tgc cgc atc acc gtc aac ggt gta gtc 336  
 Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val  
                     100                    105                    110

aag gac gaa agg atc gtc aac gaa gtg cgc gcc tat acc ttc tgc ctc 384  
 Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu  
                     115                    120                    125

gac aag tcc tca tga 399  
 Asp Lys Ser Ser  
                     130

<210> 12

<211> 132

<212> PRT

<213> Mycobacterium complex

<220>

<223> mmpS6 truncated protein

<400> 12

Leu Val Ala Val Ala Val Val Ala Val Ala Gly Phe Ser Val Tyr Arg  
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Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly  
                     20                    25                    30

Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu  
                     35                    40                    45

Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val  
                     50                    55                    60

Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr  
                     65                    70                    75                    80

Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln  
                     85                    90                    95

Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val  
                     100                    105                    110

Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu  
                     115                    120                    125

Asp Lys Ser Ser  
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<210> 13

<211> 20

<212> DNA

<213> Mycobacterium complex

<400> 13  
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<210> 14  
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<400> 15  
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<210> 17  
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<400> 18  
catagatccc ggacatggtg 20

<210> 19  
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<213> Mycobacterium canettii

<220>  
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<222> (517)..(2307)

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caacacgaac	tcgccaacg	cttagaactt	gggccgcagg	cgaaatcggt	ccagtcgccc	180
gagttcgccg	ctcgcttggc	tgccgctcaa	cacaggtagc	gcctaccagc	ctcgctgggt	240
tccatggcgt	gccccagtc	gaagctgctg	ctgcttgact	ccgcgcgctg	ggccccgagcg	300
cgcgctgttg	tacggcccaa	acggcgtgtc	ggtgtacagt	cgcgcgctcg	cggcttcagt	360
ccggcccccc	gactccggca	ggccccgacg	cgccccagcg	tagccccgaag	ttcccccttg	420
taggggcggg	ctgagtttcg	atctgtttcg	tgagcaggtg	tttctgtgtt	caacttcct	480
caacatgtac	tcatgtatta	ttgagaatag	ctcggc	gtg Val 1	tca Ser 5	tcc Ser 5
gct att atc	gcg ctg acc	gcg tgt tat	aaa gta atc	atg tac att	acc	582
Ala Ile Ile	Ala Leu Thr	Ala Cys Tyr	Lys Val Ile	Met Tyr Ile	Thr	
	10		15		20	
cgg gta ccc	aac cgg gga	tcc ccg ccg	gcg gtg ctg	ttg cgg gaa	agc	630
Arg Val Pro	Asn Arg Gly	Ser Pro Pro	Ala Val Leu	Leu Arg Glu	Ser	
	25	30		35		
ttc cgc gaa	aac ggc aag	gtc aag acg	cgt acc ctg	gcc aac ctc	tca	678
Phe Arg Glu	Asn Gly Lys	Val Lys Thr	Arg Thr Leu	Ala Asn Leu	Ser	
	40	45		50		
cgc tgg ccc	gag cac aag	ctg gac aga	ctg gac ccg	gcg cgtt aag	ggc	726
Arg Trp Pro	Glu His Lys	Leu Asp Arg	Leu Asp Arg	Ala Leu Lys	Gly	
	55	60	65		70	
ttg ccg ccc	gcg gac tgg	gat cta gcc	gag gcc ttc	gat atc acc	cg	774
Leu Pro Pro	Ala Asp Trp	Asp Leu Ala	Glu Ala Phe	Asp Ile Thr	Arg	
	75		80		85	
agc ctg ccg	cac ggg cat	gtg gcc gcg	gtg gcc ggc	acc gcc gag	aag	822
Ser Leu Pro	His Gly His	Val Ala Ala	Val Ala Gly	Thr Ala Glu	Lys	
	90	95		100		
ctg ggc ata	ccc gag ctg	atc gac ccc	acc ccg tcg	cg	cg	870
Leu Gly Ile	Pro Glu Leu	Ile Asp Pro	Thr Pro Ser	Arg Arg Arg	Asn	
	105	110		115		
ctg gtg ctg	gcc atg ctg	atc ggg cag	atc atc gag	ccc gga tcg	aaa	918
Leu Val Leu	Ala Met Leu	Ile Gly Gln	Ile Ile Glu	Pro Gly Ser	Lys	
	120	125		130		
ctg gcg atc	gcg cgc ggg	ctg cgc gcc	cag acc gcc	acc agc acg	ctg	966
Leu Ala Ile	Ala Arg Gly	Leu Arg Ala	Gln Thr Ala	Thr Ser Thr	Leu	
	135	140	145		150	
ggt gcg gtg	ctg ggt gtc	tcg ggc gcc	gat gag gac	gac ctg tat	gac	1014
Gly Ala Val	Leu Gly Val	Ser Gly Ala	Asp Glu Asp	Asp Leu Tyr	Asp	
	155		160		165	
gcg atg gac	tgg gcg ctg	gag gcg aaa	gac ggc atc	gaa aac gcc	ttg	1062
Ala Met Asp	Trp Ala Leu	Glu Arg Lys	Asp Gly Ile	Glu Asn Ala	Leu	
	170	175		180		

gcc gca cgg cat ctg acc aac ggc acc ctg gtg ctc tat gac gta tcc	1110
Ala Ala Arg His Leu Thr Asn Gly Thr Leu Val Leu Tyr Asp Val Ser	
185 190 195	
tcg gcg gcg ttc gag ggc cac acc tgc ccg ctg gga gcg atc ggg cac	1158
Ser Ala Ala Phe Glu Gly His Thr Cys Pro Leu Gly Ala Ile Gly His	
200 205 210	
gcc cgc gac ggg gtc aaa ggc ccg ctg cag atc gtc tac ggg ctg ctg	1206
Ala Arg Asp Gly Val Lys Gly Arg Leu Gln Ile Val Tyr Gly Leu Leu	
215 220 225 230	
tgc tca ccc aag gga gcg ccg gtg gcc atc gag gtg ttc aag ggc aac	1254
Cys Ser Pro Lys Gly Ala Pro Val Ala Ile Glu Val Phe Lys Gly Asn	
235 240 245	
acc gcc gac ccg aaa act ctg aaa gct caa atc gac aag ctc aaa acc	1302
Thr Ala Asp Pro Lys Thr Leu Lys Ala Gln Ile Asp Lys Leu Lys Thr	
250 255 260	
ccg ttc ggg ttg acc cgc atc gcc ctg gtg ggc gat ccg ggc atg ctc	1350
Arg Phe Gly Leu Thr Arg Ile Ala Leu Val Gly Asp Arg Gly Met Leu	
265 270 275	
act tcc gcg cgc atc cgt gac gag ctg cgt ccg gcg cac ctg gat tgg	1398
Thr Ser Ala Arg Ile Arg Asp Glu Leu Arg Pro Ala His Leu Asp Trp	
280 285 290	
atc agc gcg ctg cgc gcc ccg cag atc aag atc ctg ctc gag gac ggg	1446
Ile Ser Ala Leu Arg Ala Pro Gln Ile Lys Ile Leu Leu Glu Asp Gly	
295 300 305 310	
gcg ctg cag ctg tcg ctg ttc gat gag cag aac ctg ttc gag atc act	1494
Ala Leu Gln Leu Ser Leu Phe Asp Glu Gln Asn Leu Phe Glu Ile Thr	
315 320 325	
cac ccc gac tat ccc ggt gag ccg ctg gtg tgc tgc cac aac ccc gcc	1542
His Pro Asp Tyr Pro Gly Glu Arg Leu Val Cys Cys His Asn Pro Ala	
330 335 340	
ctg gcc gac gag cgc gcc cgc aaa cgc gcc gag ctg ctg gcg gcc acc	1590
Leu Ala Asp Glu Arg Ala Arg Lys Arg Ala Glu Leu Leu Ala Ala Thr	
345 350 355	
gaa aag gag ctg cag gcc atc gcc gaa gcc acc cgc cgc caa cgc ccg	1638
Glu Lys Glu Leu Gln Ala Ile Ala Glu Ala Thr Arg Arg Gln Arg Arg	
360 365 370	
ccg tta cgc ggt aca gac aag atc ggc ctg ccg gtg ggc aag gtg cgc	1686
Pro Leu Arg Gly Thr Asp Lys Ile Gly Leu Arg Val Gly Lys Val Arg	
375 380 385 390	
aac aag ttc aag atg gcc aag cac ttt gac ctg cac atc acc gat gag	1734
Asn Lys Phe Lys Met Ala Lys His Phe Asp Leu His Ile Thr Asp Glu	
395 400 405	
gcc ttc agc ttc acc cgc aac cag aac agt atc gcc gcc gag gcc gcc	1782
Ala Phe Ser Phe Thr Arg Asn Gln Asn Ser Ile Ala Ala Glu Ala Ala	
410 415 420	

ctc gac ggc atc tac gtg cta cgc acc agc ctg ccc gac aac gcc ctg 1830  
 Leu Asp Gly Ile Tyr Val Leu Arg Thr Ser Leu Pro Asp Asn Ala Leu  
 425 430 435

ggc cgc gac gac gtg gtg ggc cgc tac aaa gac ctc gcc gac gtc gaa 1878  
 Gly Arg Asp Asp Val Val Gly Arg Tyr Lys Asp Leu Ala Asp Val Glu  
 440 445 450

cgc ttc ttc cgc acc ctc aac agc gaa ctg gac gta cgc ccc atc cgg 1926  
 Arg Phe Phe Arg Thr Leu Asn Ser Glu Leu Asp Val Arg Pro Ile Arg  
 455 460 465 470

cat cgg ctg gcc gac cgg gtc cgc gcc cac atg ttc ttg cac atg ctc 1974  
 His Arg Leu Ala Asp Arg Val Arg Ala His Met Phe Leu His Met Leu  
 475 480 485

tcc tac tac atc agc tgg cac atg aaa caa gcc ctg gcc cca atc ctg 2022  
 Ser Tyr Tyr Ile Ser Trp His Met Lys Gln Ala Leu Ala Pro Ile Leu  
 490 495 500

ttc acc gac aac gac aaa ccc gcc gcc gcc gcc aaa cgc gcc gac ccc 2070  
 Phe Thr Asp Asn Asp Lys Pro Ala Ala Ala Lys Arg Ala Asp Pro  
 505 510 515

gtc gcg cca gcc caa cgc tcc gac gaa gcg ctg aac aag gca gca cgc 2118  
 Val Ala Pro Ala Gln Arg Ser Asp Glu Ala Leu Asn Lys Ala Ala Arg  
 520 525 530

aaa cgc acc gaa gac aac caa ccg gtg cac agc ttc acc agc ctg ctc 2166  
 Lys Arg Thr Glu Asp Asn Gln Pro Val His Ser Phe Thr Ser Leu Leu  
 535 540 545 550

acc gac ctg gcc acc atc tgc gcc aac tac atc caa ccc aca gac gac 2214  
 Thr Asp Leu Ala Thr Ile Cys Ala Asn Tyr Ile Gln Pro Thr Asp Asp  
 555 560 565

ctg cca gca ttc acc aaa acc acc acc ccc acc ccc aca caa cgg cgc 2262  
 Leu Pro Ala Phe Thr Lys Thr Thr Thr Pro Thr Pro Thr Gln Arg Arg  
 570 575 580

gcc ttc gac cta ctg gcc gtt tcc cac cgc cac ggc ctg gcg tag 2307  
 Ala Phe Asp Leu Leu Ala Val Ser His Arg His Gly Leu Ala  
 585 590 595

tcagtaccga accacaaatg cccaggtcaa cgacacaaac cgcgccggat cagggggaac 2367

ttcgggctag cccggcgcg cgc 2390

&lt;210&gt; 20

&lt;211&gt; 596

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium canettii

&lt;400&gt; 20

Val Ser Ser Ser Asp Asp Ala Ile Ile Ala Leu Thr Ala Cys Tyr Lys  
 1 5 10 15

Val Ile Met Tyr Ile Thr Arg Val Pro Asn Arg Gly Ser Pro Pro Ala  
 20 25 30

Val Leu Leu Arg Glu Ser Phe Arg Glu Asn Gly Lys Val Lys Thr Arg  
 35 40 45  
 Thr Leu Ala Asn Leu Ser Arg Trp Pro Glu His Lys Leu Asp Arg Leu  
 50 55 60  
 Asp Arg Ala Leu Lys Gly Leu Pro Pro Ala Asp Trp Asp Leu Ala Glu  
 65 70 75 80  
 Ala Phe Asp Ile Thr Arg Ser Leu Pro His Gly His Val Ala Ala Val  
 85 90 95  
 Ala Gly Thr Ala Glu Lys Leu Gly Ile Pro Glu Leu Ile Asp Pro Thr  
 100 105 110  
 Pro Ser Arg Arg Arg Asn Leu Val Leu Ala Met Leu Ile Gly Gln Ile  
 115 120 125  
 Ile Glu Pro Gly Ser Lys Leu Ala Ile Ala Arg Gly Leu Arg Ala Gln  
 130 135 140  
 Thr Ala Thr Ser Thr Leu Gly Ala Val Leu Gly Val Ser Gly Ala Asp  
 145 150 155 160  
 Glu Asp Asp Leu Tyr Asp Ala Met Asp Trp Ala Leu Glu Arg Lys Asp  
 165 170 175  
 Gly Ile Glu Asn Ala Leu Ala Ala Arg His Leu Thr Asn Gly Thr Leu  
 180 185 190  
 Val Leu Tyr Asp Val Ser Ser Ala Ala Phe Glu Gly His Thr Cys Pro  
 195 200 205  
 Leu Gly Ala Ile Gly His Ala Arg Asp Gly Val Lys Gly Arg Leu Gln  
 210 215 220  
 Ile Val Tyr Gly Leu Leu Cys Ser Pro Lys Gly Ala Pro Val Ala Ile  
 225 230 235 240  
 Glu Val Phe Lys Gly Asn Thr Ala Asp Pro Lys Thr Leu Lys Ala Gln  
 245 250 255  
 Ile Asp Lys Leu Lys Thr Arg Phe Gly Leu Thr Arg Ile Ala Leu Val  
 260 265 270  
 Gly Asp Arg Gly Met Leu Thr Ser Ala Arg Ile Arg Asp Glu Leu Arg  
 275 280 285  
 Pro Ala His Leu Asp Trp Ile Ser Ala Leu Arg Ala Pro Gln Ile Lys  
 290 295 300  
 Ile Leu Leu Glu Asp Gly Ala Leu Gln Leu Ser Leu Phe Asp Glu Gln  
 305 310 315 320  
 Asn Leu Phe Glu Ile Thr His Pro Asp Tyr Pro Gly Glu Arg Leu Val  
 325 330 335  
 Cys Cys His Asn Pro Ala Leu Ala Asp Glu Arg Ala Arg Lys Arg Ala  
 340 345 350  
 Glu Leu Leu Ala Ala Thr Glu Lys Glu Leu Gln Ala Ile Ala Glu Ala

355	360	365
Thr Arg Arg Gln Arg Arg Pro Leu Arg Gly Thr Asp Lys Ile Gly Leu 370 375 380		
Arg Val Gly Lys Val Arg Asn Lys Phe Lys Met Ala Lys His Phe Asp 385 390 395 400		
Leu His Ile Thr Asp Glu Ala Phe Ser Phe Thr Arg Asn Gln Asn Ser 405 410 415		
Ile Ala Ala Glu Ala Ala Leu Asp Gly Ile Tyr Val Leu Arg Thr Ser 420 425 430		
Leu Pro Asp Asn Ala Leu Gly Arg Asp Asp Val Val Gly Arg Tyr Lys 435 440 445		
Asp Leu Ala Asp Val Glu Arg Phe Phe Arg Thr Leu Asn Ser Glu Leu 450 455 460		
Asp Val Arg Pro Ile Arg His Arg Leu Ala Asp Arg Val Arg Ala His 465 470 475 480		
Met Phe Leu His Met Leu Ser Tyr Tyr Ile Ser Trp His Met Lys Gln 485 490 495		
Ala Leu Ala Pro Ile Leu Phe Thr Asp Asn Asp Lys Pro Ala Ala Ala 500 505 510		
Ala Lys Arg Ala Asp Pro Val Ala Pro Ala Gln Arg Ser Asp Glu Ala 515 520 525		
Leu Asn Lys Ala Ala Arg Lys Arg Thr Glu Asp Asn Gln Pro Val His 530 535 540		
Ser Phe Thr Ser Leu Leu Thr Asp Leu Ala Thr Ile Cys Ala Asn Tyr 545 550 555 560		
Ile Gln Pro Thr Asp Asp Leu Pro Ala Phe Thr Lys Thr Thr Thr Pro 565 570 575		
Thr Pro Thr Gln Arg Arg Ala Phe Asp Leu Leu Ala Val Ser His Arg 580 585 590		
His Gly Leu Ala 595		

<210> 21  
 <211> 1191  
 <212> DNA  
 <213> Mycobacterium tuberculosis  
  
 <220>  
 <221> CDS  
 <222> (1)..(1191)  
 <223> Fusion gene between mmpS6 and mmpL6 genes  
  
 <220>  
 <221> misc\_feature  
 <222> (1) (1191)

<223> CDS corresponds to fusion protein of rearranged forms  
of mmpS6 and mmpL6

<400> 1

gtg cag ggg att tca gtg act ggc ctg gtc aaa cgc ggc tgg atg gtg	48
Val Gln Gly Ile Ser Val Thr Gly Leu Val Lys Arg Gly Trp Met Val	
1 5 10 15	
aga tcc gtc ttt gac acg atc gac ggt atc gac caa ctc ggc gag cag	96
Arg Ser Val Phe Asp Thr Ile Asp Gly Ile Asp Gln Leu Gly Glu Gln	
20 25 30	
ctg gcc agc gtg acc gta acc ttg gac aag ttg gct gcg atc cag cct	144
Leu Ala Ser Val Thr Val Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro	
35 40 45	
caa ttg gtg gcg ctg cta cca gac gag atc gcc agc cag cag atc aat	192
Gln Leu Val Ala Leu Leu Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn	
50 55 60	
cgg gaa ctg gcg ctg gct aac tac gcc acc atg tcc ggg atc tat gcc	240
Arg Glu Leu Ala Leu Ala Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala	
65 70 75 80	
cag acg gcg gcc ttg atc gaa aac gct gcc gcc atg gga caa gcc ttt	288
Gln Thr Ala Ala Leu Ile Glu Asn Ala Ala Ala Met Gly Gln Ala Phe	
85 90 95	
gac gcc gcc aag aac gac gac tcc ttc tat ctg ccg ccg gag gct ttt	336
Asp Ala Ala Lys Asn Asp Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe	
100 105 110	
gac aac cca gat ttc cag cgc ggc ctg aaa ttg ttc ctg tcg gca gac	384
Asp Asn Pro Asp Phe Gln Arg Gly Leu Lys Leu Phe Leu Ser Ala Asp	
115 120 125	
ggt aag gcg gct cgg atg atc atc tcc cat gaa ggc gat ccc gcc acc	432
Gly Lys Ala Ala Arg Met Ile Ile Ser His Glu Gly Asp Pro Ala Thr	
130 135 140	
ccc gaa ggc att tcg cat atc gac gcg atc aag cag gcg gcc cac gag	480
Pro Glu Gly Ile Ser His Ile Asp Ala Ile Lys Gln Ala Ala His Glu	
145 150 155 160	
gcc gtg aag ggc act ccc atg gcg ggt gct ggg atc tat ctg gcc ggc	528
Ala Val Lys Gly Thr Pro Met Ala Gly Ala Gly Ile Tyr Leu Ala Gly	
165 170 175	
acg gcc gcc acc ttc aag gac att caa gac ggc gcc acc tac gac ctc	576
Thr Ala Ala Thr Phe Lys Asp Ile Gln Asp Gly Ala Thr Tyr Asp Leu	
180 185 190	
ctg atc gcc gga ata gcc gcg ctg agc ttg att ttg ctc atc atg atg	624
Leu Ile Ala Gly Ile Ala Ala Leu Ser Leu Ile Leu Leu Ile Met Met	
195 200 205	
atc att acc cga agc ctg gtt gcg gcg ctg gtg atc gtg ggc acg gtg	672
Ile Ile Thr Arg Ser Leu Val Ala Ala Leu Val Ile Val Gly Thr Val	
210 215 220	



gcg ctg tcg ttg ggc gct tct ttt ggc ctg tcc gtg ctg gtg tgg cag	720
Ala Leu Ser Leu Gly Ala Ser Phe Gly Leu Ser Val Leu Val Trp Gln	
225 230 235 240	
cat ctt ctc ggt atc cag ttg tac tgg atc gtg ctc gcg ctg gcc gtc	768
His Leu Leu Gly Ile Gln Leu Tyr Trp Ile Val Leu Ala Leu Ala Val	
245 250 255	
atc ctg ctc ctg gcc gtg gga tcg gac tat aac ttg ctg ctg att tcc	816
Ile Leu Leu Leu Ala Val Gly Ser Asp Tyr Asn Leu Leu Leu Ile Ser	
260 265 270	
cga ttc aag gag gag atc ggt gca ggt ttg aac acc gcc atc atc cgt	864
Arg Phe Lys Glu Glu Ile Gly Ala Gly Leu Asn Thr Gly Ile Ile Arg	
275 280 285	
gcg atg gcc ggc acc ggc ggg gtg gtg acc gct gcc ggc ctg gtg ttc	912
Ala Met Ala Gly Thr Gly Gly Val Val Thr Ala Ala Gly Leu Val Phe	
290 295 300	
gcc gcc act atg tct tcg ttc gtg ttc agt gat ttg cgg gtc ctc ggt	960
Ala Ala Thr Met Ser Ser Phe Val Phe Ser Asp Leu Arg Val Leu Gly	
305 310 315 320	
cag atc ggg acc acc att ggt ctt ggg ctg ctg ttc gac acg ctg gtg	1008
Gln Ile Gly Thr Thr Ile Gly Leu Gly Leu Leu Phe Asp Thr Leu Val	
325 330 335	
gtg cgc gcg ttc atg acc ccg tcc atc gcg gtg ctg ctc ggg cgc tgg	1056
Val Arg Ala Phe Met Thr Pro Ser Ile Ala Val Leu Leu Gly Arg Trp	
340 345 350	
ttc tgg tgg ccg caa cga gtg cgc ccg cgc cct gcc agc agg atg ctt	1104
Phe Trp Trp Pro Gln Arg Val Arg Pro Arg Pro Ala Ser Arg Met Leu	
355 360 365	
cgg ccg tac ggc ccg cgg ccc gtg gtt cgt gaa ttg ctg ctg cgc gag	1152
Arg Pro Tyr Gly Pro Arg Pro Val Val Arg Glu Leu Leu Leu Arg Glu	
370 375 380	
ggc aac gat gac ccg aga act cag gtg gct acc cac cgt	1191
Gly Asn Asp Asp Pro Arg Thr Gln Val Ala Thr His Arg	
385 390 395	

&lt;210&gt; 22

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium tuberculosis

&lt;220&gt;

&lt;223&gt; Fusion protein of rearranged forms of mmpS6 and mmpL6

&lt;400&gt; 2

Val	Gln	Gly	Ile	Ser	Val	Thr	Gly	Leu	Val	Lys	Arg	Gly	Trp	Met	Val
1					5				10					15	

Arg	Ser	Val	Phe	Asp	Thr	Ile	Asp	Gly	Ile	Asp	Gln	Leu	Gly	Glu	Gln
			20					25					30		

Leu Ala Ser Val Thr Val Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro  
 35 40 45  
 Gln Leu Val Ala Leu Leu Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn  
 50 55 60  
 Arg Glu Leu Ala Leu Ala Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala  
 65 70 75 80  
 Gln Thr Ala Ala Leu Ile Glu Asn Ala Ala Ala Met Gly Gln Ala Phe  
 85 90 95  
 Asp Ala Ala Lys Asn Asp Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe  
 100 105 110  
 Asp Asn Pro Asp Phe Gln Arg Gly Leu Lys Leu Phe Leu Ser Ala Asp  
 115 120 125  
 Gly Lys Ala Ala Arg Met Ile Ile Ser His Glu Gly Asp Pro Ala Thr  
 130 135 140  
 Pro Glu Gly Ile Ser His Ile Asp Ala Ile Lys Gln Ala Ala His Glu  
 145 150 155 160  
 Ala Val Lys Gly Thr Pro Met Ala Gly Ala Gly Ile Tyr Leu Ala Gly  
 165 170 175  
 Thr Ala Ala Thr Phe Lys Asp Ile Gln Asp Gly Ala Thr Tyr Asp Leu  
 180 185 190  
 Leu Ile Ala Gly Ile Ala Ala Leu Ser Leu Ile Leu Leu Ile Met Met  
 195 200 205  
 Ile Ile Thr Arg Ser Leu Val Ala Ala Leu Val Ile Val Gly Thr Val  
 210 215 220  
 Ala Leu Ser Leu Gly Ala Ser Phe Gly Leu Ser Val Leu Val Trp Gln  
 225 230 235 240  
 His Leu Leu Gly Ile Gln Leu Tyr Trp Ile Val Leu Ala Leu Ala Val  
 245 250 255  
 Ile Leu Leu Leu Ala Val Gly Ser Asp Tyr Asn Leu Leu Leu Ile Ser  
 260 265 270  
 Arg Phe Lys Glu Glu Ile Gly Ala Gly Leu Asn Thr Gly Ile Ile Arg  
 275 280 285  
 Ala Met Ala Gly Thr Gly Gly Val Val Thr Ala Ala Gly Leu Val Phe  
 290 295 300  
 Ala Ala Thr Met Ser Ser Phe Val Phe Ser Asp Leu Arg Val Leu Gly  
 305 310 315 320  
 Gln Ile Gly Thr Thr Ile Gly Leu Gly Leu Leu Phe Asp Thr Leu Val  
 325 330 335  
 Val Arg Ala Phe Met Thr Pro Ser Ile Ala Val Leu Leu Gly Arg Trp  
 340 345 350

Phe Trp Trp Pro Gln Arg Val Arg Pro Arg Pro Ala Ser Arg Met Leu  
355 360 365

Arg Pro Tyr Gly Pro Arg Pro Val Val Arg Glu Leu Leu Leu Arg Glu  
370 375 380

Gly Asn Asp Asp Pro Arg Thr Gln Val Ala Thr His Arg  
385 390 395